

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2002, 02:56:03 ; Search time 3106.77 Seconds  
(without alignments)  
23337.777 Million cell updates/sec

Title: US-09-652-292-1

Perfect score: 4395

Sequence: 1 gagggggtcctgcaggcc.....attatttgtaaaaaaaaaa 4395

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_om.\*

20: em\_or.\*

21: em\_ov.\*

22: em\_pat.\*

23: em\_ph.\*

24: em\_pl.\*

25: em\_ro.\*

26: em\_sts.\*

27: em\_sy.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_htgo\_hum.\*

31: em\_htgo\_inv.\*

32: em\_htgo\_rod.\*

33: em\_htg\_hum.\*

34: em\_htg\_inv.\*

35: em\_htg\_rod.\*

36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4395	100.0	4396	9	AF248053 Homo sapi
2	4105.4	93.4	4167	9	AF321240 Homo sapi
3	4064.4	92.5	4126	9	AL137188 Novel hum
4	2531.4	57.6	127418	9	AL031055 Human DNA
5	795	18.1	200125	2	AL591064 Mus muscu
6	795	18.1	243075	2	AL591805 Mus muscu
7	384.6	8.8	411	11	G31518 human STS S
8	317.4	7.2	385	6	AX150151 Sequence
9	208.6	4.7	4521	9	AB056798 Macaca fa
10	207.2	4.7	173874	2	AC068011 Homo sapi
11	201	4.6	174278	2	AC016330 Homo sapi
12	201	4.6	194958	9	AC009502 Homo sapi
13	199.8	4.5	173681	2	AL353636 Homo sapi
14	199.8	4.5	187336	9	AL158822 Human DNA
15	197.2	4.5	85378	2	AL356577 Homo sapi
16	197.2	4.5	98360	9	AL049713 Human DNA
17	196.2	4.5	117853	9	AC007030 Homo sapi
18	196	4.5	107467	9	HS95883 Homo sapien
19	195.8	4.5	160421	2	AC025005 Homo sapi
20	195.8	4.5	225022	2	AL358779 Homo sapi
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42	191.4	4.4	147430	2	AC092066 Homo chr
43	191.4	4.4	148973	2	AC092066 Homo sapi
44	191.4	4.4	167294	2	AC013814 Homo sapi
45	191.2	4.4	126801	9	AC004849 Homo sapi

## ALIGNMENTS

### RESULT 1

AF248053 4396 bp mRNA 12-APR-2001  
LOCUS Homo sapiens glucose transporter (GLUT10) mRNA, complete cds.  
DEFINITION AF248053  
ACCESSION AF248053.1 GI:13603726  
VERSION  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 4396)  
AUTHORS Fossey,S.C., Mihic,S.J., Craddock,A.L., Mychalecky,J.C.,  
Dawson,P.A. and Bowden,D.W.  
TITLE GLUT10: A novel glucose transporter in the type 2 diabetes linked  
region of chromosome 20q12-13.1  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 4396)  
AUTHORS Fossey,S.C., Mihic,S.J., Craddock,A.L., Mychalecky,J.C.,  
Dawson,P.A. and Bowden,D.W.

TITLE	Direct Submission
JOURNAL	Submitted (22-MAR-2000) Molecular Genetics, Wake Forest University, Medical Center Boulevard, Winston-Salem, NC 27106, USA
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Db 4141 ATATTACAAATAAGAGTATTTTACAAT 4167

RESULT 3
HS28H201
LOCUS
DEFINITION Novel human gene mapping to chromosome 20, similar to membrane transporters.
ACCESSION AL137188
VERSION AL137188.3 GI:11322734
KEYWORDS SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Stavrides,G.S., Hashim,Y., Huckle,E.J. and Deloukas,P.
Submitted (24-JAN-2000) E-mail contact: hunquery@sanger.ac.uk
On Nov 23, 2000 this sequence version replaced gi:11065679.
This cDNA sequence was assembled from public domain ESTs and single pass sequencing reads from expressed DNA templates, aligned to the genomic DNA sequence from the bacterial clone 2BH20 (AL031055). The EST sequences listed match this sequence with an identity of at least 95% between the coordinates shown.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20/ Sanger Centre name :
dJ28H20.C20.1.1.

FEATURES
source Location/Qualifiers
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RESULT 4  
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 LOCUS Human DNA sequence from clone RPI-28H20 on chromosome 20q13.1  
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 (facilitated glucose transporter) member 10, the 5' end of a novel  
 gene, ESTs, STSs, GSSs and three CpG Islands, complete sequence.  
 AL031055  
 ACCESSION AL031055.1 GI:4375937  
 VERSION HTG; CpG Island; SLC2A10.  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens.  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 127418)  
 REFERENCE Direct Submission  
 AUTHORS Sanger Centre, Hinxton, Hinxton, Cambridgeshire,  
 TITLE Submitted (18-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 JOURNAL CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk  
 COMMENTS requests: clonerequest@sanger.ac.uk  
 On Mar 7, 1999 this sequence version replaced gi:4056528.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 20, constructed by the Sanger Centre Chromosome 20  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr20  
 This sequence is the entire insert of clone RPI-28H20 This sequence  
 was finished as follows unless otherwise noted: all regions were  
 either double-stranded or sequenced with an alternate chemistry or  
 covered by high quality data (i.e., phred quality >= 30); an  
 attempt was made to resolve all sequencing problems, such as  
 compressions and repeats; all regions were covered by at least one  
 plasmid subclone or more than one M13 subclone; and the assembly  
 was confirmed by restriction digest. RPI-28H20 is from the library  
 RPI-1 constructed by the group of Pieter de Jong. For further  
 details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pCYPAC2.

FEATURES  
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mRNA

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1855..2079
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7023..7322
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Qy	433	tcctcgtgtgggtctctctcatctgactgctatggcaggaagaagccatctcctcgtgggagc	492
Db	164123	TCCCTTGTGGGGGCTTCCTCATTTGACTGCTATGGCAGGACGAGCCATCCTAGGGAGC	164182
Qy	493	aacttggtgctgtggcaggcagcctgacccctggcctggctgggttccctggcctggcgtg	552
Db	164183	AATCGCGTGTCTGGCTGGCAGCCCTGATCTGGGTCTGGCCAGCTCCCTGGCCCTGGGTG	164242
Qy	553	gtcctgggcgcgtgtgtgtggtctgcgaatttccctctccatggcttgcctgtgtgtatc	612
Db	164243	CTCCTGGGCCGTTTATCTGTTGGCTTGGCATCTCTCTCTTCCATGGCTTGCCTGTATC	164302
Qy	613	tacgtgtcagagctgtgtggggccacggcagcgggagtgctggttccctctatgaagca	672
Db	164303	TAGCTGTCAGAATTGGTGGGGCGCGGCAGAGGGGTGTCTGGTGTCTCCCTCTACGAGTG	164362
Qy	673	ggcatcacgtgggcactctctctctatgcccctcaacttgcactggctggttaccccc	732
Db	164363	GGCATACTGTGGGCATCTGTCTCTTACGGCTCTCACTAGCTCCTGGCTGGCAGCCCT	164422
Qy	733	tggggaTggaggcacatgttcggctgggcacgtgcacctgtgtcctgcaatccctcagc	792
Db	164423	TGGGGCTGGAGGCACATGTTTGGCTGGGCAGCTGCACCTGCTCTCCTACAGTCACTCAGC	164482
Qy	793	ctcctcttctcctcctgtgtgacagatgagactgcaaacacacaagaagacctcatccactc	852
Db	164483	CTCTTTCTTCCTCCCTGCTGTGTGAGAGGGCAGACGAGCCCCCAAGACCTTATCCCACTC	164542
Qy	853	caggaggtgagcccccgaactgtgccccggagggagccacgtactccttctctggacctc	912
Db	164543	CAGGGAAGGAGACAAACAACCGGCTGTGTGGAGCCACAGTACAGCTTCTCGACCTC	164602
Qy	913	tcagggcacgcgataacatgcgagggcccgacacagtcggcctgggctggtgtcctcttc	972
Db	164603	TTTACGGCCCCAGGACGGCATCTGGAGCCGACTGTATGTGGGCTGGGGCTGCTGCTTT	164662
Qy	973	cagcaactaacagggcagcccaacgtgtctgtctatgtctcaccatcttcaagctccggtt	1032
Db	164663	CAGCAGCTCACAGGACAGGCCAATGTCTGTATTACGCCCTCTACCACTCTTCGCTCCGTT	164722
Qy	1033	ggttccatgggggatactcagccgtgtctggcctctgtgggcttgggcagctgaagtg	1092
Db	164723	GGCTTCCACGGGGCTCCTCAGCTGTCTGTGGCTTCTGTGGGCTTGGCACGGTGAAGGTG	164782
Qy	1093	gcagctacctgaccgoccatggyggctgtgtggaccgtgcaggccgagggctctgttgcata	1152
Db	164783	GCTGCCACCTTGGTCGCCACGGGGCTGGTGGACGCTGTGACGGCGGACAGTCCCTCGCTC	164842
Qy	1153	gctggtgtacctcatgcccctgtccgttcagttggcataggccctcgtcagcttgcacctg	1212
Db	164843	TTTGGATTCGCTCTCATTGGCTTTATCGGTACGGGGCATAGGCCTGGTACGCTTTCCTGTG	164902
Qy	1213	cccatgactcagggcccaagctgtctggctgtgcccaatgcccacgggcagacagggctc	1272
Db	164903	TCCCTGGACTCTGGACCCAGCTGCCCTGGCCACATCCAAATGCCAGCCAGAGGTGGATCTG	164962
Qy	1273	cctggagactctggcctgtctgcaggactcctctctacotctcccatctccaggaccatgag	1332
Db	164963	CCTGGAAGCTCGGGTTTGTCTGTGGCTCTCATCTGCCGCCAGTGTCTACACACCAATGGG	165022

Qy	1333	gaccaaggagggacaaatcttgtgccactgtctagaataaaccaagcccatcaccagatcttgga	1392
Db	165023	GACCAAGGACAGCTGGTGCCTCAGTCACACTGAGAGA-----CCCCATCCATCCA	165070
Qy	1393	gaccttcagccccctcctcgctgcgcctgcagctgcagctccctccctgggcccctctgcgc	1452
Db	165071	GTCAATCACAGCATCCCCTGGGACCAGATTCTGAACACTGCCCTCCCGCATTTCCACACAGTCCC	165130
Qy	1453	gctcggggggatgcactgcgtgcgctggagccgcactgctgctgatgctcttttgtcagt	1512
Db	165131	ATCCTTGAGCATACCCCTGCTGCTGCTGGTCTGCCTGCTGGTTCGATGATGGTCTACCTGAGC	165190
Qy	1513	gccttcctcttgggttggccagtagaactgg	1545
Db	165191	GCCTTCCTCGGTGGCTTTGGACCAAGTAGGAGG	165223

RESULT 6  
AL591805/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

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AL591805      243075 bp      DNA          HTG           22-JUL-2001
Mus musculus chromosome 2 clone RP23-90N15, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
AL591805
AL591805.9    GI:14626203
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 243075)
Sims,S.
Direct Submission
Submitted (21-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 7, 2001 this sequence version replaced gi:14625702.
***** Genome Center *****
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
***** Project Information *****
Center project name: bm90N15
***** Summary Statistics *****
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 238544 bases at least Q40
Consensus quality: 239732 bases at least Q30
Consensus quality: 240565 bases at least Q20
Insert size: 241575; sum-of-contigs
Insert size: 239393; 4.9% error; agarose-fp
Quality coverage: 8.35x in Q20 bases; sum-of-contigs Quality
coverage: 8.51x in Q20 bases; agarose-fp
*****
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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FEATURES

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1..45622  
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misc\_feature  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 411)  
 AUTHORS Myers, R.M.  
 JOURNAL Unpublished (1997)  
 COMMENT  
 Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu  
 Primer A: ACTATCACTGCGATTGGCC  
 Primer B: GCGGACCTATACCCATTCT  
 STS size: 100  
 PCR Profile:  
 Initial incubation: 94 degrees C for 90 seconds  
 Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30  
 Thermal Cycler: Perkin Elmer 9600  
 Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul  
 Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3  
 Prepared with primer pairs provided by Sandoz, derived from N93207  
 -- Washington University/Merck EST sequence.  
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 /map="20"  
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 primer\_bind complement(388..407)  
 BASE COUNT 134 a 60 c 49 g 164 t 4 others  
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 Query Match 8.8%; Score 384.6; DB 11; Length 411;  
 Best Local Similarity 97.8%; Pred. No. 1e-62;  
 Matches 398; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
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 Db 411 TCATGCGGACCTATACCCATTCTTCAGGCGCTAGCTGTACA-WTATCAGGAGATTTTAT 353  
 QY 4049 tcgtagtctaatcttgcataatcgccaaatcgccagtgatgtgactttggatacaa 4108  
 Db 352 TCCTAGTCTAATTTTGTCAAATCATGCGCAATCGCAGTGATGCTGACTTTGGATACAA 293  
 QY 4109 ggtttggcaaaaaaaataattacaataattctctgtaagaatcaattggctatgga 4168  
 Db 292 GGTTCGCAAAAAAATAATTAACNAAATATTCTGTAAGAATCAATTGGCTATATGGA 233  
 QY 4169 atttagataaagaattttacaataagaattttacaataagaattttattatttt 4228  
 Db 232 ATTTAGGATAAGAAATATTTCNCAATAAAGAAATTTTCNCAATAAAGAGTTTATTATTATTT 173

QY 4229 gtaagttgtgcacaaacataccctttatctctgttaaaattttacacacaaaaatta 4288  
 Db 172 GTAAGTTGTGAGCAACAAACATACCCTTTCTCTGTAAAAATTTATACACAAAAATTA 113  
 QY 4289 acaaaagattctgtaagaatttaattgctatatatggaatttaggataagaattttacata 4348  
 Db 112 ACAAAGATTCTGTAAGAAATTAATTTGGCTATATGGAATTTAGGATAGAAATTTTACAATA 53  
 QY 4349 aagagattttacaataaagagtttggatttattatttgcataaaaaa 4395  
 Db 52 AAGAGTATTACAAATAAAGAGTTTGTATTATTATTGTTAAATAAAAAAAA 6

## RESULT 8

AX150151/c

LOCUS

AX150151

DEFINITION

Sequence 126 from Patent WO0136685.

ACCESSION

AX150151

VERSION

AX150151.1

GI:14348179

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 385)

AUTHORS

Kroes, R.A., Moskal, J.R. and Yamamoto, H.

TITLE

Differential gene expression in cancer

JOURNAL

Patent: WO 0136685-A 126 25-MAY-2001;

NYXIS Neurotherapies, Inc. (US)

FEATURES

Location/Qualifiers

source 1..385

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 127 a 61 c 43 g 154 t

ORIGIN

Query Match

Best Local Similarity

7.2%; Score 317.4; DB 6; Length 385;

Matches 344; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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Db 373 TCCGAGCTGTACAGTTATTCAGGGATTTTATTGTTAGTCTAAATTTGTCAAATCATGGC 314

QY 4077 caaatccagtgatgttgcttggatcacaggtttggc-aaaaaaataattaca 4135

Db 313 CAAATCCGGTGATAGTTGATTTGGATACAGGTTTGGCAAAAAAATAAATATTATACA 254

QY 4136 aaattctctgtaagaatcaattggctatatggaatttaggataagaattttacaataa 4195

Db 253 AATATTCTGTAGAAATCAATTTGCTATATGGAATTTAGGATAAAGA--ATTACAATAA 196

QY 4196 agaattattacaataaagagttttattattatttcgtagttgtgtgcaacaataccct 4255

Db 195 AGAATATTACAAATAAAGAGTTTATTATTATTGTTAGTGTGTGCAACAACATACCT 136

QY 4256 ttatctctgtaaaattttacacacaaaaatacaaaagattctctgtaagaattttatgg 4315

Db 135 TTATCTCTGTAAAAATTTATACACAAAAAATAAATAAAGATTTCTGTAAAGAAATTAATGG 76

QY 4316 ctatatggaatttaggataagaattttacaataaagagttatttacaataaaga 4368

Db 75 CTATATGGAATTTAGGATAGAAATTTTACAATAAAGAGTATTTACAATAAATAA 23

## RESULT 9

AB056798

LOCUS

AB056798

DEFINITION

Macaca fascicularis brain cDNA clone:QfLA-11110, full insert

ACCESSION

AB056798



AB056798.1 GI:133658996  
 fis (full insert sequence); oligo capping.  
 Macaca fascicularis adult male frontal lobe left cDNA to mRNA,  
 clone\_lib:macaque brain cDNA library OF1a clone:OF1a-11110.  
 Macaca fascicularis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 1 (sites)  
 Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,  
 Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.  
 Isolation of full-length cDNA clones from macaque brain cDNA  
 libraries  
 Unpublished  
 2 (bases 1 to 4521)  
 Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.  
 Direct Submission  
 Submitted (09-MAR-2001) Katsuyuki Hashimoto, National Institute of  
 Infectious Diseases, Division of Genetic Resources; 23-1, Toyama  
 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
 (E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,  
 Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)  
 Lab host: TOP10  
 Vector: pME18S-FL3 (Acc.No. AB009864)  
 R. Site1: DraIII (CACTGTGTG)  
 R. Site2: DraIII (CACCATGTG)  
 Description: 1st strand cDNA was primed with an oligo(dT) primer  
 using specific 5' and 3' primers and amplified by PCR. The PCR  
 product was digested with SfiI and size selection was performed to  
 exclude fragments <1.5kb. The SfiI-digested PCR product was cloned  
 into distinct DraIII sites of pME18S-FL3. XhoI sites just outside  
 the DraIII sites can be used to isolate the cDNA insert. Libraries  
 were constructed by Sugano et al.(University of Tokyo, Institute of  
 Medical Science). Custom primer used for sequencing  
 ( 5' end primer [CTGTGCTCTAAAGCTGG];  
 3' end primer [CGACCTGCAGCTCGACACA] ).  
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 /db\_xref="taxon:9541"  
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 /sex="male"  
 /tissue\_type="frontal lobe left"  
 /clone\_lib="macaque brain cDNA library OF1a"  
 /dev\_stage="adult"  
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 R. Site1: DraIII (CACTGTGTG); R. Site2: DraIII  
 (CACCATGTG)"  
 157..2022  
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 ETAPQRRGLLVSLNEMVILGILSAYISNFAVFWKMGVGLVIFLIGLQIAIAM  
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 TIPATLLVDSGKNTFLCIGISVMAALVTMGIVNLNHNFTICRSHNSINQSLDE  
 SVIYQGNLSNPNTRLDHFQGIASHSRSSIMPLRNDVDKRGETTSSALINVLHSRTE  
 YQITVDGQDVPAFLKWLISLILVVAFAFGISGLGPMPLWLSIEFFPGGIRGRAMLTS  
 SNWNGINLLISITFTVTDILGLRQWCFITITMSLASLFLVNMFIPTETKGSLEQISM  
 ELAKVNVKNNITFTMSHDEELVPRQKRRKPOQLLECNKLCGRGQSRQLSPEN"  
 1340 a 943 c 920 g 1318 t

BASE COUNT  
 1340 a 943 c 920 g 1318 t

ORIGIN

Query Match 4.7%; Score 208.6; DB 9; Length 4521;  
 Best Local Similarity 49.5%; Pred. No. 1.2e-29;  
 Matches 760; Conservative 0; Mismatches 709; Indels 66; Gaps 6;











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      /clone_lib="RPC1-11.1"
      62..505
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      742..2258
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      2259..2562
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      2563..4145
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      5757..6067
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      6089..6419
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      6420..6895
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      10950..11254
      /note="AluSc repeat: matches 1..305 of consensus"

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Search completed: March 15, 2002, 05:49:46  
Job time: 10423 sec